

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: NATIONAL VETERINARY INSTITUTE
- (B) STREET: P.O. Box 7073
- (C) CITY: UPPSALA
- (E) COUNTRY: SWEDEN
- (F) POSTAL CODE (ZIP): 750 07
- (G) TELEPHONE: +46 18 67 40 00
- (H) TELEFAX: +46 18 30 91 62

(ii) TITLE OF INVENTION: MITE PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAA GCG GAA GTT ACG TTC TCC GAT AGT GAA GAT AAG AAA AAT TAT TTC	48
Glu Ala Glu Val Thr Phe Ser Asp Ser Glu Asp Lys Lys Asn Tyr Phe	
1 5 10 15	
GTC GAA CTT AAA AAA GAT AAA GAT TTA TAT TCG ATG AAA TCG AAT GTG	96
Val Glu Leu Lys Lys Asp Lys Asp Leu Tyr Ser Met Lys Ser Asn Val	
20 25 30	
AAA CGA AAC AAT GAG ATT TTC TAT GAG AAC AAT ATG GAT TTG GAG AAG	144
Lys Arg Asn Asn Glu Ile Phe Tyr Glu Asn Asn Met Asp Leu Glu Lys	
35 40 45	

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AAC GGT AAA ATG AAT TGG TAT TAC AAA CGA AAC GAT CGA ACA TGG AAT Asn Gly Lys Met Asn Trp Tyr Tyr Lys Arg Asn Asp Arg Thr Trp Asn 50 55 60	192
ATG GAT CTC GAT AAT GCA TTC AAT CCA AGA GAT GGT ACA ATG AAA CTT Met Asp Leu Asp Asn Ala Phe Asn Pro Arg Asp Gly Thr Met Lys Leu 65 70 75 80	240
CAA GTG AAA GAT CGT ATC TAT GAT ATC AAA TTG AAA CGA GAA CCG TTC Gln Val Lys Asp Arg Ile Tyr Asp Ile Lys Leu Lys Arg Glu Pro Phe 85 90 95	288
CGA TAC GGT GAT CTA CAT ATC GAA GGA AAT GAG AAT CCT TTG ATC AAA Arg Tyr Gly Asp Leu His Ile Glu Gly Asn Glu Asn Pro Leu Ile Lys 100 105 110	336
AAG GGT GAT TTA CAT ATG TCT CTC GTC GAT CCG CTT ACT TTG AAT GTT Lys Gly Asp Leu His Met Ser Leu Val Asp Pro Leu Thr Leu Asn Val 115 120 125	384
TTG ACC AAG AAT GAT GGA ATC GTC GAT ATG ACA TTG GAT TTG GTC TCT Leu Thr Lys Asn Asp Gly Ile Val Asp Met Thr Leu Asp Leu Val Ser 130 135 140	432
CCC AAC ACC AAA AAA GCA GCG CTA AAA ATC AAT TCG AAA AAA TAC GAT Pro Asn Thr Lys Lys Ala Ala Leu Lys Ile Asn Ser Lys Lys Tyr Asp 145 150 155 160	480
CTT GAT CAT GAT GGT GAG ATT ACC GTT TCG ATC TTT AAT CCT CGA ATG Leu Asp His Asp Gly Glu Ile Thr Val Ser Ile Phe Asn Pro Arg Met 165 170 175	528
ACT TGG AAA CAT CAC ACT AGA AAA GGT GAT ATG GAA TTG AAT ATT GAT Thr Trp Lys His His Thr Arg Lys Gly Asp Met Glu Leu Asn Ile Asp 180 185 190	576
GCT GAT ATC ACT CGA AAA GGT TCA TTG ATC ACC TAT TT CGT AAA GAG Ala Asp Ile Thr Arg Lys Gly Ser Leu Ile Thr Tyr Ser Arg Lys Glu 195 200 205	624
CCA GAT GAT TCG ACA AAA GTT CGA TAT TCA AGA CAA GGA AAT CAA GTT Pro Asp Asp Ser Thr Lys Val Arg Tyr Ser Arg Gln Gly Asn Gln Val 210 215 220	672
TCG ATG GAA GTC GAT TCT AAA TTG ATC GAA GGC CAT GCG AAC GAA ACT Ser Met Glu Val Asp Ser Lys Leu Ile Glu Gly His Ala Asn Gly Thr 225 230 235 240	720
TTG ACC GAT GGC AAA ATT CAT GTC AAA GGT CGA GAG AGT GAT TTC AA Leu Thr Asp Gly Lys Ile His Val Lys Gly Arg Glu Ser Asp Phe Gu 245 250 255	768
ATC GAA AGC ACC TAT AAA GTT GAA GAT GGT AAG CTT ATG ATT GAG CCA Ile Glu Ser Thr Tyr Lys Val Glu Asp Gly Lys Leu Met Ile Glu Pro 260 265 270	816
ACC AAA ACT CAG AAT GGA AAA TTA GAA GGT CTT CTT TCG AGA AAA GTA Thr Lys Thr Gln Asn Gly Lys Leu Glu Gly Leu Leu Ser Arg Lys Val 275 280 285	864

CCA TCA CAT CTT GTT CTT GAA ACA CCA AGA GTG AAA ATG AAC ATG AAA 912
 Pro Ser His Leu Val Leu Glu Thr Pr Arg Val Lys Met Asn Met Lys
 290 295 300

TAT GAT AGA TTT GCT CCG GTG AAG ATA TTG AAA TTA GAT TAC GAT GGT 960
 Tyr Asp Arg Phe Ala Pro Val Lys Ile Leu Lys Leu Asp Tyr Asp Gly
 305 310 315 320

TTG AAT TAT GAG AAA CAT ATC GAT GCT GAA TAC GAG CCA TCA AAT CAT 1008
 Leu Asn Tyr Glu Lys His Ile Asp Ala Glu Tyr Glu Pro Ser Asn His
 325 330 335

TAC AAA TAC TTT ACC GAT GGT AAA TCG AAG AGA AGT GGC AAA GGT TAT 1056
 Tyr Lys Tyr Phe Thr Asp Gly Lys Ser Lys Arg Ser Gly Lys Gly Tyr
 340 345 350

TCG ATC AAA ATC GAT GGA AAA CCA AAG AAA GCA TTG AAA GTT GAT GTC 1104
 Ser Ile Lys Ile Asp Gly Lys Pro Lys Lys Ala Leu Lys Val Asp Val
 355 360 365

GAT ATG CCG GAT TTT AAA TTC AAT GTG AAC AAA CCG GAA GAT AGT AAC 1152
 Asp Met Pro Asp Phe Lys Phe Asn Val Asn Lys Pro Glu Asp Ser Asn
 370 375 380

AAA GCT CAA TTT AGT TAT ACA TTC AAT GAT TAT ACC GAA ACG GAA GAG 1200
 Lys Ala Gln Phe Ser Tyr Thr Phe Asn Asp Tyr Thr Glu Thr Glu Glu
 385 390 395 400

TAT GAA TTC GAT CCA CAT CGT GCA TAT ATC TTG AAT TGG GCC AGA GCT 1248
 Tyr Glu Phe Asp Pro His Arg Ala Tyr Ile Leu Asn Trp Ala Arg Ala
 405 410 415

ATC AGA CAA TAT TTG CAG ACA TTC ATT GTT GAG TAG 1284
 Ile Arg Gln Tyr Leu Gln Thr Phe Ile Val Glu *
 420 425

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Glu Ala Glu Val Thr Phe Ser Asp Ser Glu Asp Lys Lys Asn Tyr Phe
 1 5 10 15

Val Glu Leu Lys Lys Asp Lys Asp Leu Tyr Ser Met Lys Ser Asn Val
 20 25 30

Lys Arg Asn Asn Glu Ile Phe Tyr Glu Asn Asn Met Asp Leu Glu Lys
 35 40 45

Asn Gly Lys Met Asn Trp Tyr Tyr Lys Arg Asn Asp Arg Thr Trp Asn
 50 55 60

Met Asp Leu Asp Asn Ala Phe Asn Pro Arg Asp Gly Thr Met Lys Leu
 65 70 75 80

Gln Val Lys Asp Arg Ile Tyr Asp Ile Lys Leu Lys Arg Glu Pro Phe
 85 90 95
 Arg Tyr Gly Asp Leu His Ile Glu Gly Asn Glu Asn Pro Leu Ile Lys
 100 105 110
 Lys Gly Asp Leu His Met Ser Leu Val Asp Pro Leu Thr Leu Asn Val
 115 120 125
 Leu Thr Lys Asn Asp Gly Ile Val Asp Met Thr Leu Asp Leu Val Ser
 130 135 140
 Pro Asn Thr Lys Lys Ala Ala Leu Lys Ile Asn Ser Lys Lys Tyr Asp
 145 150 155 160
 Leu Asp His Asp Gly Glu Ile Thr Val Ser Ile Phe Asn Pro Arg Met
 165 170 175
 Thr Trp Lys His His Thr Arg Lys Gly Asp Met Glu Leu Asn Ile Asp
 180 185 190
 Ala Asp Ile Thr Arg Lys Gly Ser Leu Ile Thr Tyr Ser Arg Lys Glu
 195 200 205
 Pro Asp Asp Ser Thr Lys Val Arg Tyr Ser Arg Gln Gly Asn Gln Val
 210 215 220
 Ser Met Glu Val Asp Ser Lys Leu Ile Glu Gly His Ala Asn Gly Thr
 225 230 235 240
 Leu Thr Asp Gly Lys Ile His Val Lys Gly Arg Glu Ser Asp Phe Glu
 245 250 255
 Ile Glu Ser Thr Tyr Lys Val Glu Asp Gly Lys Leu Met Ile Glu Pro
 260 265 270
 Thr Lys Thr Gln Asn Gly Lys Leu Glu Gly Leu Leu Ser Arg Lys Val
 275 280 285
 Pro Ser His Leu Val Leu Glu Thr Pro Arg Val Lys Met Asn Met Lys
 290 295 300
 Tyr Asp Arg Phe Ala Pro Val Lys Ile Leu Lys Leu Asp Tyr Asp Gly
 305 310 315 320
 Leu Asn Tyr Glu Lys His Ile Asp Ala Glu Tyr Glu Pro Ser Asn His
 325 330 335
 Tyr Lys Tyr Phe Thr Asp Gly Lys Ser Lys Arg Ser Gly Lys Gly Tyr
 340 345 350
 Ser Ile Lys Ile Asp Gly Lys Pro Lys Lys Ala Leu Lys Val Asp Val
 355 360 365
 Asp Met Pr Asp Phe Lys Phe Asn Val Asn Lys Pro Glu Asp Ser Asn
 370 375 380
 Lys Ala Gln Phe Ser Tyr Thr Phe Asn Asp Tyr Thr Glu Thr Glu Glu
 385 390 395 400

FOUO 254450

Tyr Glu Phe Asp Pro His Arg Ala Tyr Ile Leu Asn Trp Ala Arg Ala
405 410 415

Ile Arg Gln Tyr Leu Gln Thr Phe Ile Val Glu *
420 425

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ser Arg Cys Asp Leu Gln His His His His His His
1 5 10

FOOTNOTES

SEQUENCE LISTING

<110> MATTSSON, JENS

<120> MITE PROTEIN

<130> 53631-65307

<140> 09/914,352

<141> 2000-02-22

<150> PCT/SE00/00346

<151> 2000-02-22

<150> SE 9900674-4

<151> 1999-02-25

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 1284

<212> DNA

<213> Sarcoptes scabiei

<220>

<221> CDS

<222> (1)..(1281)

<400> 1

gaa gcg gaa gtt acg ttc tcc gat agt gaa gat aag aaa aat tat ttc	48
Glu Ala Glu Val Thr Phe Ser Asp Ser Glu Asp Lys Lys Asn Tyr Phe	
1 5 10 15	
gtc gaa ctt aaa aaa gat aaa gat tta tat tcg atg aaa tcg aat gtg	96
Val Glu Leu Lys Lys Asp Lys Asp Leu Tyr Ser Met Lys Ser Asn Val	
20 25 30	
aaa cga aac aat gag att ttc tat gag aac aat atg gat ttg gag aag	144
Lys Arg Asn Asn Glu Ile Phe Tyr Glu Asn Asn Met Asp Leu Glu Lys	
35 40 45	
aac ggt aaa atg aat tgg tat tac aaa cga aac gat cga aca tgg aat	192
Asn Gly Lys Met Asn Trp Tyr Tyr Lys Arg Asn Asp Arg Thr Trp Asn	
50 55 60	
atg gat ctc gat aat gca ttc aat cca aga gat ggt aca atg aaa ctt	240
Met Asp Leu Asp Asn Ala Phe Asn Pro Arg Asp Gly Thr Met Lys Leu	
65 70 75 80	
caa gtg aaa gat cgt atc tat gat atc aaa ttg aaa cga gaa cgg ttc	288
Gln Val Lys Asp Arg Ile Tyr Asp Ile Lys Leu Lys Arg Glu Arg Phe	
85 90 95	
cga tac ggt gat cta cat atc gaa gga aat gag aat cct ttg atc aaa	336
Arg Tyr Gly Asp Leu His Ile Glu Gly Asn Glu Asn Pro Leu Ile Lys	
100 105 110	

aag ggt gat tta cat atg tct ctc gtc gat ccg ctt act ttg aat gtt	384
Lys Gly Asp Leu His Met Ser Leu Val Asp Pro Leu Thr Leu Asn Val	
115 120 125	
ttg acc aag aat gat gga atc gtc gat atg aca ttg gat ttg gtc tct	432
Leu Thr Lys Asn Asp Gly Ile Val Asp Met Thr Leu Asp Leu Val Ser	
130 135 140	
ccc aac acc aaa aaa gca gcg cta aaa atc aat tcg aaa aaa tac gat	480
Pro Asn Thr Lys Lys Ala Ala Leu Lys Ile Asn Ser Lys Lys Tyr Asp	
145 150 155 160	
ctt gat cat gat ggt gag att acc gtt tcg atc ttt aat cct cga atg	528
Leu Asp His Asp Gly Glu Ile Thr Val Ser Ile Phe Asn Pro Arg Met	
165 170 175	
act tgg aaa cat cac act aga aaa ggt gat atg gaa ttg aat att gat	576
Thr Trp Lys His His Thr Arg Lys Gly Asp Met Glu Leu Asn Ile Asp	
180 185 190	
gct gat atc act cga aaa ggt tca ttg atc acc tat tct cgt aaa gag	624
Ala Asp Ile Thr Arg Lys Gly Ser Leu Ile Thr Tyr Ser Arg Lys Glu	
195 200 205	
cca gat gat tcg aca aaa gtt cga tat tca aga caa gga aat caa gtt	672
Pro Asp Asp Ser Thr Lys Val Arg Tyr Ser Arg Gln Gly Asn Gln Val	
210 215 220	
tcg atg gaa gtc gat tct aaa ttg atc gaa ggc cat gcg aac gga act	720
Ser Met Glu Val Asp Ser Lys Leu Ile Glu Gly His Ala Asn Gly Thr	
225 230 235 240	
ttg acc gat ggc aaa att cat gtc aaa ggt cga gag agt gat ttc gaa	768
Leu Thr Asp Gly Lys Ile His Val Lys Gly Arg Glu Ser Asp Phe Glu	
245 250 255	
atc gaa agc acc tat aaa gtt gaa gat ggt aag ctt atg att gag cca	816
Ile Glu Ser Thr Tyr Lys Val Glu Asp Gly Lys Leu Met Ile Glu Pro	
260 265 270	
acc aaa act cag aat gga aaa tta gaa ggt ctt ctt tcg aga aaa gta	864
Thr Lys Thr Gln Asn Gly Lys Leu Glu Gly Leu Leu Ser Arg Lys Val	
275 280 285	
cca tca cat ctt gtt ctt gaa aca cca aga gtg aaa atg aac atg aaa	912
Pro Ser His Leu Val Leu Glu Thr Pro Arg Val Lys Met Asn Met Lys	
290 295 300	
tat gat aga ttt gct ccg gtg aag ata ttg aaa tta gat tac gat ggt	960
Tyr Asp Arg Phe Ala Pro Val Lys Ile Leu Lys Leu Asp Tyr Asp Gly	
305 310 315 320	
ttg aat tat gag aaa cat atc gat gct gaa tac gag cca tca aat cat	1008
Leu Asn Tyr Glu Lys His Ile Asp Ala Glu Tyr Glu Pro Ser Asn His	
325 330 335	

tac aaa tac ttt acc gat ggt aaa tcg aag aga agt ggc aaa ggt tat 1056
 Tyr Lys Tyr Phe Thr Asp Gly Lys Ser Lys Arg Ser Gly Lys Gly Tyr
 340 345 350

tcg atc aaa atc gat gga aaa cca aag aaa gca ttg aaa gtt gat gtc 1104
 Ser Ile Lys Ile Asp Gly Lys Pro Lys Lys Ala Leu Lys Val Asp Val
 355 360 365

gat atg ccg gat ttt aaa ttc aat gtg aac aaa ccg gaa gat agt aac 1152
 Asp Met Pro Asp Phe Lys Phe Asn Val Asn Lys Pro Glu Asp Ser Asn
 370 375 380

aaa gct caa ttt agt tat aca ttc aat gat tat acc gaa acg gaa gag 1200
 Lys Ala Gln Phe Ser Tyr Thr Phe Asn Asp Tyr Thr Glu Thr Glu Glu
 385 390 395 400

tat gaa ttc gat cca cat cgt gca tat atc ttg aat tgg gcc aga gct 1248
 Tyr Glu Phe Asp Pro His Arg Ala Tyr Ile Leu Asn Trp Ala Arg Ala
 405 410 415

atc aga caa tat ttg cag aca ttc att gtt gag tag 1284
 Ile Arg Gln Tyr Leu Gln Thr Phe Ile Val Glu
 420 425

<210> 2

<211> 427

<212> PRT

<213> *Sarcoptes scabiei*

<400> 2

Glu Ala Glu Val Thr Phe Ser Asp Ser Glu Asp Lys Lys Asn Tyr Phe
 1 5 10 15

Val Glu Leu Lys Lys Asp Lys Asp Leu Tyr Ser Met Lys Ser Asn Val
 20 25 30

Lys Arg Asn Asn Glu Ile Phe Tyr Glu Asn Asn Met Asp Leu Glu Lys
 35 40 45

Asn Gly Lys Met Asn Trp Tyr Tyr Lys Arg Asn Asp Arg Thr Trp Asn
 50 55 60

Met Asp Leu Asp Asn Ala Phe Asn Pro Arg Asp Gly Thr Met Lys Leu
 65 70 75 80

Gln Val Lys Asp Arg Ile Tyr Asp Ile Lys Leu Lys Arg Glu Arg Phe
 85 90 95

Arg Tyr Gly Asp Leu His Ile Glu Gly Asn Glu Asn Pro Leu Ile Lys
 100 105 110

Lys Gly Asp Leu His Met Ser Leu Val Asp Pro Leu Thr Leu Asn Val
 115 120 125

Leu Thr Lys Asn Asp Gly Ile Val Asp Met Thr Leu Asp Leu Val Ser
 130 135 140

Pro Asn Thr Lys Lys Ala Ala Leu Lys Ile Asn Ser Lys Lys Tyr Asp
 145 150 155 160
 Leu Asp His Asp Gly Glu Ile Thr Val Ser Ile Phe Asn Pro Arg Met
 165 170 175
 Thr Trp Lys His His Thr Arg Lys Gly Asp Met Glu Leu Asn Ile Asp
 180 185 190
 Ala Asp Ile Thr Arg Lys Gly Ser Leu Ile Thr Tyr Ser Arg Lys Glu
 195 200 205
 Pro Asp Asp Ser Thr Lys Val Arg Tyr Ser Arg Gln Gly Asn Gln Val
 210 215 220
 Ser Met Glu Val Asp Ser Lys Leu Ile Glu Gly His Ala Asn Gly Thr
 225 230 235 240
 Leu Thr Asp Gly Lys Ile His Val Lys Gly Arg Glu Ser Asp Phe Glu
 245 250 255
 Ile Glu Ser Thr Tyr Lys Val Glu Asp Gly Lys Leu Met Ile Glu Pro
 260 265 270
 Thr Lys Thr Gln Asn Gly Lys Leu Glu Gly Leu Leu Ser Arg Lys Val
 275 280 285
 Pro Ser His Leu Val Leu Glu Thr Pro Arg Val Lys Met Asn Met Lys
 290 295 300
 Tyr Asp Arg Phe Ala Pro Val Lys Ile Leu Lys Leu Asp Tyr Asp Gly
 305 310 315 320
 Leu Asn Tyr Glu Lys His Ile Asp Ala Glu Tyr Glu Pro Ser Asn His
 325 330 335
 Tyr Lys Tyr Phe Thr Asp Gly Lys Ser Lys Arg Ser Gly Lys Gly Tyr
 340 345 350
 Ser Ile Lys Ile Asp Gly Lys Pro Lys Lys Ala Leu Lys Val Asp Val
 355 360 365
 Asp Met Pro Asp Phe Lys Phe Asn Val Asn Lys Pro Glu Asp Ser Asn
 370 375 380
 Lys Ala Gln Phe Ser Tyr Thr Phe Asn Asp Tyr Thr Glu Thr Glu Glu
 385 390 395 400
 Tyr Glu Phe Asp Pro His Arg Ala Tyr Ile Leu Asn Trp Ala Arg Ala
 405 410 415
 Ile Arg Gln Tyr Leu Gln Thr Phe Ile Val Glu
 420 425

<210> 3

<211> 12

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 3
 Ser Arg Cys Asp Leu Gln His His His His His His
 1 5 10

<210> 4
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 4
 cactatcgga gaacgtaact tcgg

24

<210> 5
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
 cctggcattc tacttgagat gta

23

<210> 6
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
 cgctctagac tcaacaatga atgtctgcaa

30

<210> 7
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 7
 cgggatccga atatttcgtc tcgaaaccg

29